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RAW SEQUENCE LISTING

DATE: 11/14/2001

PATENT APPLICATION: US/09/918,508

TIME: 15:06:24

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Output Set: N:\CRF3\11142001\I918508.raw

3 <110> APPLICANT: KAKIMOTO, TATSUO
 4 HIGUCHI, MASAYUKI
 5 INOUE, TSUTOMU
 7 <120> TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY
 8 TO CYTOKININ RECEPTOR
 10 <130> FILE REFERENCE: Q65478
 12 <140> CURRENT APPLICATION NUMBER: 09/918,508
 13 <141> CURRENT FILING DATE: 2001-08-01
 15 <150> PRIOR APPLICATION NUMBER: JP 2001-073812
 16 <151> PRIOR FILING DATE: 2001-03-15
 18 <160> NUMBER OF SEQ ID NOS: 22
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 3531
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Arabidopsis thaliana
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (1)..(3531)
 31 <400> SEQUENCE: 1

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34	1 5 10 15	
36	aag tcg tcg agc agt gac aag aaa tgg cta aag aag cct ctc ttc ttc	96
37	Lys Ser Ser Ser Ser Asp Lys Lys Trp Leu Lys Lys Pro Leu Phe Phe	
38	20 25 30	
40	ctg att ttg tgt ggc tct ttg gta att gtt ttg gtt atg ttc tta cgg	144
41	Leu Ile Leu Cys Gly Ser Leu Val Ile Val Leu Val Met Phe Leu Arg	
42	35 40 45	
44	tta ggt aga agt cag aag gag gag aca gat tct tgt aat gga gaa gag	192
45	Leu Gly Arg Ser Gln Lys Glu Glu Thr Asp Ser Cys Asn Gly Glu Glu	
46	50 55 60	
48	aaa gtg ttg tat aga cat caa aat gtc aca aga agt gag att cat gat	240
49	Lys Val Leu Tyr Arg His Gln Asn Val Thr Arg Ser Glu Ile His Asp	
50	65 70 75 80	
52	ttg gtc tct ttg ttc tct gat tca gat cag gta aca tcc ttt gaa tgt	288
53	Leu Val Ser Leu Phe Ser Asp Ser Asp Gln Val Thr Ser Phe Glu Cys	
54	85 90 95	
56	cat aag gaa tca agc cct gga atg tgg aca aac tat ggt att aca tgt	336
57	His Lys Glu Ser Ser Pro Gly Met Trp Thr Asn Tyr Gly Ile Thr Cys	
58	100 105 110	
60	tcc ctg agt gtg cgt tct gat aaa caa gag act aga ggg ctt ccc tgg	384
61	Ser Leu Ser Val Arg Ser Asp Lys Gln Glu Thr Arg Gly Leu Pro Trp	
62	115 120 125	
64	aat ctt ggc tta gga cat tct atc tca tca aca tct tgt atg tgt ggt	432
65	Asn Leu Gly Leu Gly His Ser Ile Ser Ser Thr Ser Cys Met Cys Gly	
66	130 135 140	

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70	145					150					155					160	
72	cat	gaa	gaa	ggg	ctg	gag	cag	ggt	ttg	tca	tcg	tat	tta	aga	aat	gca	528
73	His	Glu	Glu	Gly	Leu	Glu	Gln	Gly	Leu	Ser	Ser	Tyr	Leu	Arg	Asn	Ala	
74					165					170						175	
76	tgg	tgg	tgt	cta	atc	ctt	ggt	gtg	tta	gtg	tgc	cat	aag	att	tat	gta	576
77	Trp	Trp	Cys	Leu	Ile	Leu	Gly	Val	Leu	Val	Cys	His	Lys	Ile	Tyr	Val	
78				180					185					190			
80	tct	cat	tct	aaa	gca	cga	ggt	gag	agg	aaa	gag	aaa	gta	cat	ctg	caa	624
81	Ser	His	Ser	Lys	Ala	Arg	Gly	Glu	Arg	Lys	Glu	Lys	Val	His	Leu	Gln	
82			195					200					205				
84	gag	gct	tta	gct	cca	aag	aag	cag	caa	caa	cgt	gct	cag	act	tct	tct	672
85	Glu	Ala	Leu	Ala	Pro	Lys	Lys	Gln	Gln	Gln	Arg	Ala	Gln	Thr	Ser	Ser	
86		210					215				220						
88	aga	ggg	gct	gga	aga	tgg	agg	aag	aat	atc	ctt	ctc	ctt	ggt	att	tta	720
89	Arg	Gly	Ala	Gly	Arg	Trp	Arg	Lys	Asn	Ile	Leu	Leu	Leu	Gly	Ile	Leu	
90	225					230				235						240	
92	gga	gga	gtt	tcc	ttc	tct	gtt	tgg	tgg	ttt	tgg	gac	act	aat	gag	gag	768
93	Gly	Gly	Val	Ser	Phe	Ser	Val	Trp	Trp	Phe	Trp	Asp	Thr	Asn	Glu	Glu	
94				245						250					255		
96	atc	ata	atg	aaa	agg	agg	gag	act	ttg	gca	aac	atg	tgt	gac	gaa	cga	816
97	Ile	Ile	Met	Lys	Arg	Arg	Glu	Thr	Leu	Ala	Asn	Met	Cys	Asp	Glu	Arg	
98				260					265					270			
100	gca	cgt	gtt	tta	caa	gat	cag	ttc	aat	gtt	agc	ttg	aac	cat	gtt	cat	864
101	Ala	Arg	Val	Leu	Gln	Asp	Gln	Phe	Asn	Val	Ser	Leu	Asn	His	Val	His	
102			275					280					285				
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105	Ala	Leu	Ser	Ile	Leu	Val	Ser	Thr	Phe	His	His	Gly	Lys	Ile	Pro	Ser	
106		290					295					300					
108	gcc	att	gat	cag	aga	aca	ttt	gaa	gaa	tat	act	gag	aga	aca	aac	ttt	960
109	Ala	Ile	Asp	Gln	Arg	Thr	Phe	Glu	Glu	Tyr	Thr	Glu	Arg	Thr	Asn	Phe	
110	305					310				315					320		
112	gag	agg	cca	ctt	act	agt	ggt	gta	gcg	tat	gct	ttg	aaa	gtc	cca	cac	1008
113	Glu	Arg	Pro	Leu	Thr	Ser	Gly	Val	Ala	Tyr	Ala	Leu	Lys	Val	Pro	His	
114				325						330					335		
116	tca	gaa	aga	gag	aaa	ttt	gaa	aag	gag	cat	gga	tgg	gca	ata	aag	aaa	1056
117	Ser	Glu	Arg	Glu	Lys	Phe	Glu	Lys	Glu	His	Gly	Trp	Ala	Ile	Lys	Lys	
118			340						345					350			
120	atg	gaa	act	gag	gac	cag	aca	gtt	gta	caa	gat	tgt	gtt	cct	gaa	aac	1104
121	Met	Glu	Thr	Glu	Asp	Gln	Thr	Val	Val	Gln	Asp	Cys	Val	Pro	Glu	Asn	
122			355					360					365				
124	ttt	gat	ccc	gca	ccg	att	caa	gac	gaa	tac	gcg	cca	gtt	ata	ttt	gct	1152
125	Phe	Asp	Pro	Ala	Pro	Ile	Gln	Asp	Glu	Tyr	Ala	Pro	Val	Ile	Phe	Ala	
126		370					375					380					
128	caa	gaa	act	gtt	tcc	cat	att	gta	tcg	gtc	gac	atg	atg	tct	gga	gaa	1200
129	Gln	Glu	Thr	Val	Ser	His	Ile	Val	Ser	Val	Asp	Met	Met	Ser	Gly	Glu	
130	385					390					395					400	
132	gaa	gac	cgt	gaa	aac	atc	tta	cgg	gca	agg	gca	tca	gga	aaa	gga	gtg	1248

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136	tta	aca	tct	cca	ttt	aag	ctt	ctt	aag	tca	aat	cat	ctt	ggt	gtt	gtg	1296
137	Leu	Thr	Ser	Pro	Phe	Lys	Leu	Leu	Lys	Ser	Asn	His	Leu	Gly	Val	Val	
138				420					425					430			
140	ttg	acc	ttt	gct	gtc	tat	gac	acg	agc	cta	ccg	cct	gat	gct	aca	gaa	1344
141	Leu	Thr	Phe	Ala	Val	Tyr	Asp	Thr	Ser	Leu	Pro	Pro	Asp	Ala	Thr	Glu	
142			435					440					445				
144	gaa	cag	cgt	gtt	gaa	gca	act	att	ggg	tac	ctt	ggt	gca	tca	tat	gat	1392
145	Glu	Gln	Arg	Val	Glu	Ala	Thr	Ile	Gly	Tyr	Leu	Gly	Ala	Ser	Tyr	Asp	
146		450					455					460					
148	atg	cca	tcg	ctg	gtg	gag	aaa	ctt	ctt	cac	caa	ctt	gcc	agc	aaa	cag	1440
149	Met	Pro	Ser	Leu	Val	Glu	Lys	Leu	Leu	His	Gln	Leu	Ala	Ser	Lys	Gln	
150	465					470				475					480		
152	aca	att	gct	gtg	gat	gtt	tac	gac	aca	act	aac	act	tca	ggt	cta	ata	1488
153	Thr	Ile	Ala	Val	Asp	Val	Tyr	Asp	Thr	Thr	Asn	Thr	Ser	Gly	Leu	Ile	
154				485					490					495			
156	aaa	atg	tat	ggc	tca	gaa	att	ggg	gat	ata	agt	gag	cag	cat	ata	agt	1536
157	Lys	Met	Tyr	Gly	Ser	Glu	Ile	Gly	Asp	Ile	Ser	Glu	Gln	His	Ile	Ser	
158			500					505					510				
160	agc	ctt	gat	ttt	ggt	gat	cca	tca	agg	aac	cat	gag	atg	cat	tgc	agg	1584
161	Ser	Leu	Asp	Phe	Gly	Asp	Pro	Ser	Arg	Asn	His	Glu	Met	His	Cys	Arg	
162			515				520					525					
164	ttt	aag	cat	aaa	ctt	ccc	att	ccc	tgg	aca	gcg	ata	aca	ccg	tcg	atc	1632
165	Phe	Lys	His	Lys	Leu	Pro	Ile	Pro	Trp	Thr	Ala	Ile	Thr	Pro	Ser	Ile	
166		530				535				540							
168	tta	gtt	ctg	gtt	att	act	ttt	ctt	gtt	ggt	tat	att	tta	tat	gaa	gcc	1680
169	Leu	Val	Leu	Val	Ile	Thr	Phe	Leu	Val	Gly	Tyr	Ile	Leu	Tyr	Glu	Ala	
170	545				550				555				560				
172	atc	aac	cga	att	gcg	aca	gtt	gaa	gag	gat	tgt	cag	aag	atg	agg	gaa	1728
173	Ile	Asn	Arg	Ile	Ala	Thr	Val	Glu	Glu	Asp	Cys	Gln	Lys	Met	Arg	Glu	
174				565				570					575				
176	ctc	aaa	gct	cgt	gct	gag	gcc	gct	gac	att	gca	aag	tca	cag	ttc	cta	1776
177	Leu	Lys	Ala	Arg	Ala	Glu	Ala	Ala	Asp	Ile	Ala	Lys	Ser	Gln	Phe	Leu	
178				580				585					590				
180	gca	act	gtt	tct	cat	gag	ata	cgg	act	ccg	atg	aat	gga	gtt	tta	gga	1824
181	Ala	Thr	Val	Ser	His	Glu	Ile	Arg	Thr	Pro	Met	Asn	Gly	Val	Leu	Gly	
182			595					600					605				
184	atg	ctg	aaa	atg	ctg	atg	gac	acc	gat	ctt	gat	gcg	aag	cag	atg	gac	1872
185	Met	Leu	Lys	Met	Leu	Met	Asp	Thr	Asp	Leu	Asp	Ala	Lys	Gln	Met	Asp	
186		610				615						620					
188	tat	gcg	caa	act	gct	cat	ggc	agt	ggg	aag	gat	ctt	aca	tca	cta	ata	1920
189	Tyr	Ala	Gln	Thr	Ala	His	Gly	Ser	Gly	Lys	Asp	Leu	Thr	Ser	Leu	Ile	
190	625				630				635				640				
192	aat	gag	gtt	ctt	gat	cag	gca	aag	att	gaa	tcc	gga	agg	ctc	gag	ctt	1968
193	Asn	Glu	Val	Leu	Asp	Gln	Ala	Lys	Ile	Glu	Ser	Gly	Arg	Leu	Glu	Leu	
194				645				650					655				
196	gaa	aat	gtg	cct	ttt	gat	atg	cgt	ttt	att	ctt	gat	aat	gtt	tca	tct	2016
197	Glu	Asn	Val	Pro	Phe	Asp	Met	Arg	Phe	Ile	Leu	Asp	Asn	Val	Ser	Ser	

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202		675		680		685		
204	gtt tct agt	caa gtt cct	gat gtt gta gtc	ggt gat ccg	agt cgg ttc	2112		
205	Val Ser Ser	Gln Val Pro	Asp Val Val	Val Gly Asp	Pro Ser Arg	Phe		
206		690		695		700		
208	cgg cag atc	att aca aac	ctg gtt gga aac	tca atc aaa	ttc aca cag	2160		
209	Arg Gln Ile	Ile Thr Asn	Leu Val Gly	Asn Ser Ile	Lys Phe Thr	Gln		
210	705		710		715		720	
212	gaa agg gga	cac ata ttt	atc tca gtg	cac ctt gca	gat gag gta	aag	2208	
213	Glu Arg Gly	His Ile Phe	Ile Ser Val	His Leu Ala	Asp Glu Val	Lys		
214		725		730		735		
216	gag cct ctt	act att gaa	gac gca gtg	cta aaa cag	cga cta gct	tta	2256	
217	Glu Pro Leu	Thr Ile Glu	Asp Ala Val	Leu Lys Gln	Arg Leu Ala	Leu		
218		740		745		750		
220	gga tgc agc	gag tcc ggt	gag aca gtt	agc ggg ttt	cct gcg gta	aat	2304	
221	Gly Cys Ser	Glu Ser Gly	Glu Thr Val	Ser Gly Phe	Pro Ala Val	Asn		
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224	gca tgg gga	agc tgg aag	aat ttc aag	aca tgt tac	agt act gag	agt	2352	
225	Ala Trp Gly	Ser Trp Lys	Asn Phe Lys	Thr Cys Tyr	Ser Thr Glu	Ser		
226		770		775		780		
228	cag aat tct	gat caa atc	aaa ttg cta	gtt aca gtg	gag gac act	gga	2400	
229	Gln Asn Ser	Asp Gln Ile	Lys Leu Leu	Val Thr Val	Glu Asp Thr	Gly		
230	785		790		795		800	
232	gtt ggc ata	cct gtg gat	gca caa ggc	cga atc ttc	aca cct ttt	atg	2448	
233	Val Gly Ile	Pro Val Asp	Ala Gln Gly	Arg Ile Phe	Thr Pro Phe	Met		
234		805		810		815		
236	caa gcc gac	agt tcc aca	tcg cgg act	tat ggt gga	act ggc ata	ggt	2496	
237	Gln Ala Asp	Ser Ser Thr	Ser Arg Thr	Tyr Gly Gly	Thr Gly Ile	Gly		
238		820		825		830		
240	ttg agt ata	agc aaa cgt	ttg gtt gaa	ctc atg caa	gga gag atg	ggg	2544	
241	Leu Ser Ile	Ser Lys Arg	Leu Val Glu	Leu Met Gln	Gly Glu Met	Gly		
242		835		840		845		
244	ttt gtg agt	gag ccc ggg	ata ggc agt	act ttt tca	ttt act gga	gtt	2592	
245	Phe Val Ser	Glu Pro Gly	Ile Gly Ser	Thr Phe Ser	Phe Thr Gly	Val		
246		850		855		860		
248	ttc ggg aaa	gca gaa aca	aat acg tcg	att act aag	ctg gaa cga	ttc	2640	
249	Phe Gly Lys	Ala Glu Thr	Asn Thr Ser	Ile Thr Lys	Leu Glu Arg	Phe		
250	865		870		875		880	
252	gat cta gct	att cag gag	ttt aca gga	ttg aga gca	tta gtt att	gat	2688	
253	Asp Leu Ala	Ile Gln Glu	Phe Thr Gly	Leu Arg Ala	Leu Val Ile	Asp		
254		885		890		895		
256	aac aga aac	att aga gca	gag gtc acc	agg tac gaa	ctt cgg aga	ctg	2736	
257	Asn Arg Asn	Ile Arg Ala	Glu Val Thr	Arg Tyr Glu	Leu Arg Arg	Leu		
258		900		905		910		
260	gga ata tct	gca gac att	gtt tca agt	ctg aga atg	gca tgc act	tgt	2784	
261	Gly Ile Ser	Ala Asp Ile	Val Ser Ser	Leu Arg Met	Ala Cys Thr	Cys		
262		915		920		925		

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265 Cys Ile Ser Lys Leu Glu Asn Leu Ala Met Ile Leu Ile Asp Lys Asp
266 930 935 940
268 gcc tgg aac aag gaa gaa ttt tca gta ctt gac gag ttg ttt acc cga 2880
269 Ala Trp Asn Lys Glu Glu Phe Ser Val Leu Asp Glu Leu Phe Thr Arg
270 945 950 955 960
272 agc aaa gta acc ttt aca aga gtc cca aag att ttt ctt ttg gca act 2928
273 Ser Lys Val Thr Phe Thr Arg Val Pro Lys Ile Phe Leu Leu Ala Thr
274 965 970 975
276 tct gca act ctt act gag cgc agt gag atg aag tct act ggt ctc atc 2976
277 Ser Ala Thr Leu Thr Glu Arg Ser Glu Met Lys Ser Thr Gly Leu Ile
278 980 985 990
280 gat gag gtg gtg ata aag cct ctt cgg atg agt gtc tta ata tgt tgc 3024
281 Asp Glu Val Val Ile Lys Pro Leu Arg Met Ser Val Leu Ile Cys Cys
282 995 1000 1005
284 ttg caa gaa acc ctt gtc aat ggc aag aag agg caa ccg aac aga cag 3072
285 Leu Gln Glu Thr Leu Val Asn Gly Lys Lys Arg Gln Pro Asn Arg Gln
286 1010 1015 1020
288 cga aga aat ctt gga cac ttg cta aga gaa aaa cag att ctg gtt gtg 3120
289 Arg Arg Asn Leu Gly His Leu Leu Arg Glu Lys Gln Ile Leu Val Val
290 1025 1030 1035 1040
292 gat gat aat ctt gtg aac aga cga gtt gca gaa ggt gca ctt aag aaa 3168
293 Asp Asp Asn Leu Val Asn Arg Arg Val Ala Glu Gly Ala Leu Lys Lys
294 1045 1050 1055
296 tat gga gct att gtt aca tgc gtt gag agt ggc aaa gct gca ttg gca 3216
297 Tyr Gly Ala Ile Val Thr Cys Val Glu Ser Gly Lys Ala Ala Leu Ala
298 1060 1065 1070
300 atg ctt aag ccg cct cat aac ttc gat gct tgc ttc atg gat ctc cag 3264
301 Met Leu Lys Pro Pro His Asn Phe Asp Ala Cys Phe Met Asp Leu Gln
302 1075 1080 1085
304 atg cct gaa atg gat gga ttt gaa gcg aca agg aga gtc cgt gag ctg 3312
305 Met Pro Glu Met Asp Gly Phe Glu Ala Thr Arg Arg Val Arg Glu Leu
306 1090 1095 1100
308 gag agg gaa atc aat aag aaa ata gct tct gga gaa gtt tca gct gaa 3360
309 Glu Arg Glu Ile Asn Lys Lys Ile Ala Ser Gly Glu Val Ser Ala Glu
310 1105 1110 1115 1120
312 atg ttc tgt aaa ttt agt agt tgg cac gtc ccg ata tta gca atg aca 3408
313 Met Phe Cys Lys Phe Ser Ser Trp His Val Pro Ile Leu Ala Met Thr
314 1125 1130 1135
316 gca gat gtt att cag gct act cat gaa gaa tgc atg aaa tgt gga atg 3456
317 Ala Asp Val Ile Gln Ala Thr His Glu Glu Cys Met Lys Cys Gly Met
318 1140 1145 1150
320 gat ggt tat gta tca aaa ccg ttt gaa gag gaa gtg ctc tac aca gcg 3504
321 Asp Gly Tyr Val Ser Lys Pro Phe Glu Glu Glu Val Leu Tyr Thr Ala
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329 <210> SEQ ID NO: 2

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